ClinVar

NCBI's ClinVar is a freely available submission-driven database for information about genomic variation and its relationship to human health.

ClinVar accepts submissions interpretations of genetic data from:

- **clinical genetics testing laboratories**
- **research groups**
- **expert panels**
- **and others**

Interpret your data and guide your diagnosis
ncbi.nlm.nih.gov/clinvar

- **1,670+ submitters**
- **75+ countries**
- **841,000+ variants**
- **1,300,000+ submitted records**
- **ClinVar Search Video**

Contact us at clinvar@ncbi.nlm.nih.gov

Follow us on Twitter @ncbi_clinical

Visit us at ncbi.nlm.nih.gov/clinvar/ to find out more

National Library of Medicine
National Center for Biotechnology Information

ClinVar aggregates
clinical assertions about variants provided by clinical genetics testing laboratories
and others.

ClinVar helps clinicians
interpret genetic test results
and diagnose disorders to
improve patient outcomes.

What's New

Automated validation in the ClinVar submission portal for quick resolution of common errors and faster submission processing time

Submit to ClinVar

Submit Now

1. **Setup and register** – Review ClinVar Submission Guide for details, including how to create your myncbi account and register your organization
2. **Submit** – Use the submission wizard for a single variant submission or excel, TSV/CSV, or XML formats for multiple submissions
3. **Review and access** – Your data will be available on ClinVar after curatorial review and processing

Download

Download Now

- The comprehensive dataset in XML, aggregated either by variant or by variant-disease pairs
- A summary of ClinVar data in VCF format
- A summary of ClinVar data, and other more specific slices of data, as tab-delimited files

dbGaP

An NIH-sponsored repository for archiving, curating, and distributing information produced by genome-scale studies investigating the interaction of human genotype and phenotype

Augment your research

View Map

Over
2.6 million
research subjects

Over
1,500 research studies

Over
350,000 variables

Over
100,000
samples of non-genomics omics data

Over
400,000
whole genome and whole exome sequences related to dbGaP studies, available on Amazon Web Services and Google Cloud

dbGaP study submission steps (NIH funded studies)

1 Registration

- Contact NIH Program Officer or Genomic Program Administrator (GPA)
- Receive invitation
- Enter study metadata

2 Submission

- Use dbGaP submission guide to upload files
- Work with curators to complete submission
- Get accession number

3 Release

- Approve processed data
- Release study

Submit Now

Upcoming

- Public API for study metadata and controlled-access data access using FHIR (Fast Healthcare Interoperability Resources) protocol
- Automated validation in dbGaP Submission Portal for quick feedback and shorter submission processing timeframes

dbGaP study access steps (for Principal Investigators (PIs)

1 Account Setup

- NIH Intramural researchers – submit permission form to establish data request eligibility in dbGaP
- Other researchers – Get eRA commons user account

2 Access Application

- Complete / revise and submit application to Signing Officer (SO)
- SO certifies application with one or more Data Access Requests (DAR)

3 Approval and Access

- dbGaP Data Access Committee (DAC) reviews and approves application
- dbGaP approved data is provided for download

MedGen

Medical genetics information at your fingertips, aggregated from your favorite resources!

ACCESS RESOURCES

Embed links in your EHR or clinical software pipeline to bring your users the latest genetic disease and phenotype data and analytics tools from authoritative sources

USE IDENTIFIERS

Use MedGen as your source for mapped genetic disease names and identifiers from HPO, MONDO, OMIM, UMLS, and others, to enable linking across resources

STREAMLINE SUBMISSIONS

MedGen is the phenotype backbone of ClinVar and GTR. Facilitate your organization's submissions by using the disease identifiers in MedGen

RESOURCES

MedGen supports research, diagnosis and treatment of genetic disorders by providing information on:

- Mendelian disorders
- Pharmacogenetic responses
- Complex diseases
- Clinical findings

TOOLS

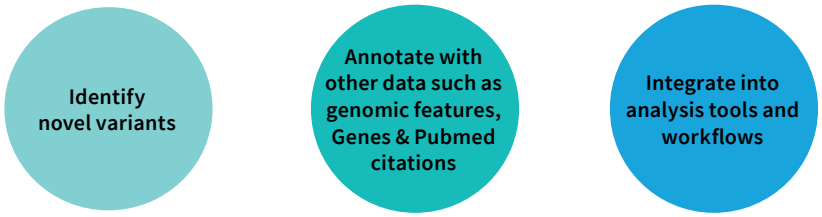
MedGen's all-in-one platform connects clinicians to leading genetic resources, including:

- PubMed
- GARD
- GeneReviews®
- OMIM

Visit MedGen

Variation Resources

NCBI's variation resources offer human genomic variations, including common and rare SNV, other small-scale variations, large structural variations, and associated frequencies, including ALFA, a new aggregated frequency source based on data from millions of controlled-access research study subjects. Access through the web, APIs, and FTP downloads.



dbSNP

Visit dbSNP

- Over 2 Billion submissions including data from 1000 Genomes, GnomAD, and others
- 720 Million RS
- Frequency for more than 606 Million RS; including common and rare variants
- Rich annotation reported on RefSeq GRCH37 and GRCH38 assemblies, mRNA, and Protein
- VCF files for assemblies GRCh37 and GRCh38
- Full set of RefSNPs in the JSON format
- Indexed Search

dbVar

Visit dbVar

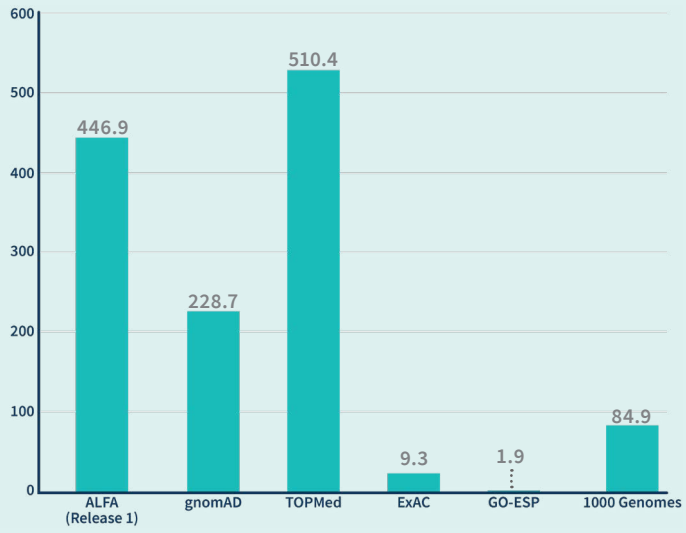
- 193 studies
- Clinically significant SV, Case-Control, and Curated Datasets
- 6.0 million unique structural variants
- 36.1 million submitted variant calls
- Updated monthly
- Population allele frequency
- Files are available in XML, GVF, VCF, BED, BEDPE, and TSV for assemblies GRCh37 and GRCh38
- dbVar Tutorials and Datasets
- Access full set of FTP files

ALFA

Visit ALFA

- Release 1 (March 2020) included 447M variants from 98K subjects
- Release 2 (October 2020) will include an additional ~100K subjects for a total of ~200K
- Access ALFA data along with other projects including GnomAD, and TOPMed

Variants with frequency data (by project in, million)



Variation Services

Web services for comparing, normalizing, annotating, and inter-converting variations

Visit Now

Variation Viewer

View, search, and navigate variations in genomic context. Review data or upload your own data

Visit Now